Errors Corrected by the STIC S●oms Branch

Serial Number: _09/242,657B_

ENTERED

CRF Processing Date: _2/6/2001_
Edited by: _____
Verified by: _M.____ (STIC staff

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TECH CENTER 1600/2900

#15

- [ ] / Changed a file from non-ASCII to ASCII

- [x] / Changed the margins in cases where the sequence text was "wrapped" down to the next line.

- [ ] Edited a format error in the Current Application Data section, specifically: _____

- [ ] Edited the Current Application Data section with the actual current number. The number inputted by the applicant was [ ] the prior application data; or [ ] other _____.

- [ ] Added the mandatory heading and subheadings for "Current Application Data".

- [ ] Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

- [ ] Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____

- [ ] Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____

- [ ] Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____

- [ ] Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

- [ ] Inserted colons after headings/subheadings. Headings edited included: _____

- [ ] Deleted extra, invalid, headings used by an applicant, specifically: _____

- [ ] Deleted: [ ] non-ASCII "garbage" at the beginning/end of files; [ ] secretary initials/filename at end of file; [ ] page numbers throughout text; [ ] other invalid text, such as_____

- [ ] Inserted mandatory headings, specifically: _____

- [ ] Corrected an obvious error in the response, specifically: _____

- [ ] Edited identifiers where upper case is used but lower case is required, or vice versa.

- [ ] Corrected an error in the Number of Sequences field, specifically: _____

- [ ] A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

- [ ] Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

- [ ] Other: _____

_____

_____

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

Input Set : A:\Sequence Listing (55411.2).txt
Output Set: N:\CRF3\02062001\I242657B.raw

```
537          (D) OTHER INFORMATION:/standard_name=
538 "Constitutional promoter"
539 /label= Cp15
541          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
543 CATTACNTAG TTNATTCTTG ACAGAATTAC GATTCGCTGG TATAATATAT
544 CAGTACTGTT 60
546 (2) INFORMATION FOR SEQ ID NO: 12:
548     (i) SEQUENCE CHARACTERISTICS:
549          (A) LENGTH: 58 base pairs
550          (B) TYPE: nucleic acid
551          (C) STRANDEDNESS: double
552          (D) TOPOLOGY: linear
554     (ii) MOLECULE TYPE: DNA (genomic)
556     (iii) HYPOTHETICAL: YES
558     (iv) ANTI-SENSE: NO
560     (vi) ORIGINAL SOURCE:
561          (A) ORGANISM: Lactococcus lactis
563     (ix) FEATURE:
564          (A) NAME/KEY: promoter
565          (B) LOCATION:4..58
566          (D) OTHER INFORMATION:/standard_name=
567 "Constitutional promoter"
568 /label= Cp16
570          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
572 CATTGTGTAG TTTATTCTTG ACAGCTATGA GTCAATTTGG TATAATAACA
573 GTACTCAG 58
575 (2) INFORMATION FOR SEQ ID NO: 13:
577     (i) SEQUENCE CHARACTERISTICS:
578          (A) LENGTH: 59 base pairs
579          (B) TYPE: nucleic acid
580          (C) STRANDEDNESS: double
581          (D) TOPOLOGY: linear
583     (ii) MOLECULE TYPE: DNA (genomic)
585     (iii) HYPOTHETICAL: YES
587     (iv) ANTI-SENSE: NO
589     (vi) ORIGINAL SOURCE:
590          (A) ORGANISM: Lactococcus lactis
592     (ix) FEATURE:
593          (A) NAME/KEY: promoter
594          (B) LOCATION:4..59
595          (D) OTHER INFORMATION:/standard_name=
596 "Constitutional promoter"
597 /label= Cp17
599          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
601 CATTCTGGAG TTTATTCTTG ACCGCTCAGT ATGCAGTGGT ATAATAGTAC
602 AGTACTGTT 59
604 (2) INFORMATION FOR SEQ ID NO: 14:
606     (i) SEQUENCE CHARACTERISTICS:
607          (A) LENGTH: 58 base pairs
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E--> 543
E--> 572
E--> 601

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608            (B) TYPE: nucleic acid
609            (C) STRANDEDNESS: double
610            (D) TOPOLOGY: linear
612      (ii) MOLECULE TYPE: DNA (genomic)
614     (iii) HYPOTHETICAL: YES
616      (iv) ANTI-SENSE: NO
618      (vi) ORIGINAL SOURCE:
619            (A) ORGANISM: Lactococcus lactis
621      (ix) FEATURE:
622            (A) NAME/KEY: promoter
623            (B) LOCATION:4..58
624            (D) OTHER INFORMATION:/standard_name=
625 "Constitutional promoter"
626 /label= Cp18
628      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
E--> 630 CATTTTGCAG TTTATTCTTG ACATTGTGTG CTTCGGGTGT ATAATACTAA
631 GTACTGTT 58
633 (2) INFORMATION FOR SEQ ID NO: 15:
635      (i) SEQUENCE CHARACTERISTICS:
636            (A) LENGTH: 58 base pairs
637            (B) TYPE: nucleic acid
638            (C) STRANDEDNESS: double
639            (D) TOPOLOGY: linear
641      (ii) MOLECULE TYPE: DNA (genomic)
643     (iii) HYPOTHETICAL: YES
645      (iv) ANTI-SENSE: NO
647      (vi) ORIGINAL SOURCE:
648            (A) ORGANISM: Lactococcus lactis
650      (ix) FEATURE:
651            (A) NAME/KEY: promoter
652            (B) LOCATION:4..58
653            (D) OTHER INFORMATION:/standard_name=
654 "Constitutional promoter"
655 /label= Cp19
657      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:
E--> 659 CATCGCTTAG TTTTTCTTGA CAGGAGGGAT CCGGGTTGAT ATAATAGTTA
660 GTACTGTT 58
662 (2) INFORMATION FOR SEQ ID NO: 16:
664      (i) SEQUENCE CHARACTERISTICS:
665            (A) LENGTH: 60 base pairs
666            (B) TYPE: nucleic acid
667            (C) STRANDEDNESS: double
668            (D) TOPOLOGY: linear
670      (ii) MOLECULE TYPE: DNA (genomic)
672     (iii) HYPOTHETICAL: YES
674      (iv) ANTI-SENSE: NO
676      (vi) ORIGINAL SOURCE:
677            (A) ORGANISM: Lactococcus lactis
679      (ix) FEATURE:
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751       (i) SEQUENCE CHARACTERISTICS:
752            (A) LENGTH: 60 base pairs
753            (B) TYPE: nucleic acid
754            (C) STRANDEDNESS: double
755            (D) TOPOLOGY: linear
757      (ii) MOLECULE TYPE: DNA (genomic)
759     (iii) HYPOTHETICAL: YES
761      (iv) ANTI-SENSE: NO
763      (vi) ORIGINAL SOURCE:
764            (A) ORGANISM: Lactococcus lactis
766      (ix) FEATURE:
767            (A) NAME/KEY: promoter
768            (B) LOCATION:4..60
769            (D) OTHER INFORMATION:/standard_name=
770 "Constitutional promoter"
771 /label= Cp23
772      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:
E--> 773 CATGTAGGAG TTTATTCTTG ACAGATTAGT TAGGGGGTGG TATAATATCT
774 CAGTACTGTT 60
776 (2) INFORMATION FOR SEQ ID NO: 20:
778       (i) SEQUENCE CHARACTERISTICS:
779            (A) LENGTH: 60 base pairs
780            (B) TYPE: nucleic acid
781            (C) STRANDEDNESS: double
782            (D) TOPOLOGY: linear
784      (ii) MOLECULE TYPE: DNA (genomic)
786     (iii) HYPOTHETICAL: YES
788      (iv) ANTI-SENSE: NO
790      (vi) ORIGINAL SOURCE:
791            (A) ORGANISM: Lactococcus lactis
793      (ix) FEATURE:
794            (A) NAME/KEY: promoter
795            (B) LOCATION:4..60
796            (D) OTHER INFORMATION:/standard_name=
797 "Constitutional promoter"
798 /label= Cp24
800      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:
E--> 802 CATGGGTAAG TTTATTCTTC ACACTATCTG GGCCCGATGG TATAATAAGT
803 GACTACTGTT 60
805 (2) INFORMATION FOR SEQ ID NO: 21:
807       (i) SEQUENCE CHARACTERISTICS:
808            (A) LENGTH: 59 base pairs
809            (B) TYPE: nucleic acid
810            (C) STRANDEDNESS: double
811            (D) TOPOLOGY: linear
813      (ii) MOLECULE TYPE: DNA (genomic)
815     (iii) HYPOTHETICAL: YES
817      (iv) ANTI-SENSE: NO
819      (vi) ORIGINAL SOURCE:
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 820            (A) ORGANISM: Lactococcus lactis
 822      (ix) FEATURE:
 823            (A) NAME/KEY: promoter
 824            (B) LOCATION:3..59
 825            (D) OTHER INFORMATION:/standard_name=
 826 "Constitutional promoter"
 827 /label= Cp25
 828       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:
E--> 830 CTTTGGCAGT TTATTCTTGA CATGTAGTGA GGGGGCTGGT ATAATCACAT
 831 AGTACTGTT 59
1484 (2) INFORMATION FOR SEQ ID NO: 43:
1486      (i) SEQUENCE CHARACTERISTICS:
1487            (A) LENGTH: 177 base pairs
1488            (B) TYPE: nucleic acid
1489            (C) STRANDEDNESS: double
1490            (D) TOPOLOGY: linear
1492     (ii) MOLECULE TYPE: DNA (genomic)
1494    (iii) HYPOTHETICAL: YES
1496     (iv) ANTI-SENSE: NO
1498     (vi) ORIGINAL SOURCE:
1499            (A) ORGANISM: Saccharomyces cerevisiae
1501      (ix) FEATURE:
1502            (A) NAME/KEY: promoter
1503            (B) LOCATION:8..177
1504            (C) IDENTIFICATION METHOD: experimental
1505            (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
1506 /standard_name= "Yeast promoter"
1507 /label= Yp102
1508      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:
E--> 1510 GAATTCGTGA CTCAAACGGG TGGTCGACGG GTGGTTCCAA TTAATTGGCG
1511 TCCCTCTTAT        60
E--> 1513 AAAGGCGAGG GTACGTGCGA CAATTGGTAG AGCGAGCGGG GCTCTTAAGT
1514 GCAAGTGACT        120
E--> 1516 GCGAACATTT TTTTCGTTTG TTAGAATAAT TCAAGAATCG CTACCAATCA TGGATCC
W--> 1517 177
1520 (2) INFORMATION FOR SEQ ID NO: 44:
1522      (i) SEQUENCE CHARACTERISTICS:
1523            (A) LENGTH: 182 base pairs
1524            (B) TYPE: nucleic acid
1525            (C) STRANDEDNESS: double
1526            (D) TOPOLOGY: linear
1528     (ii) MOLECULE TYPE: DNA (genomic)
1530    (iii) HYPOTHETICAL: YES
1532     (iv) ANTI-SENSE: NO
1534     (vi) ORIGINAL SOURCE:
1535            (A) ORGANISM: Saccharomyces cerevisiae
1537      (ix) FEATURE:
1538            (A) NAME/KEY: promoter
1539            (B) LOCATION:8..181
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       1540          (C) IDENTIFICATION METHOD: experimental
       1541          (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
       1542 /standard_name= "Yeast promoter"
       1543 /label= Yp112
       1545      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:
E--> 1547 GAATTCGTGA CTCACGGCAT CTGATGGTTG ACCATAGTCA GGAACATTGT
       1548 GCTGGAGTTC         60
E--> 1550 CTTGAGGAAT GAGTTATAAA ATGGGAGGTT GCGGCTAATG CCAGGCAGGA
       1551 GAGGAACCCT        120
E--> 1553 CTTAAGTGCA AGTGACTGCA AACATTTTTT TCGTTTGTTG AATCGCTACC
       1554 AATCATGGAT        180
E--> 1556 CC
W--> 1557 182
       1560 (2) INFORMATION FOR SEQ ID NO: 45:
       1562      (i) SEQUENCE CHARACTERISTICS:
       1563          (A) LENGTH: 191 base pairs
       1564          (B) TYPE: nucleic acid
       1565          (C) STRANDEDNESS: double
       1566          (D) TOPOLOGY: linear
       1568     (ii) MOLECULE TYPE: DNA (genomic)
       1570    (iii) HYPOTHETICAL: YES
       1572     (iv) ANTI-SENSE: NO
       1574     (vi) ORIGINAL SOURCE:
       1575          (A) ORGANISM: Saccharomyces cerevisiae
       1577     (ix) FEATURE:
       1578          (A) NAME/KEY: promoter
       1579          (B) LOCATION:8..181
       1580          (C) IDENTIFICATION METHOD: experimental
       1581          (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
       1582 /standard_name= "Yeast promoter"
       1583 /label= Yp13
       1585      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:
E--> 1587 GAATTCGTGA CTCACTAGGC AGGTCACGTT GGCTCTTCGC GGCGCAGGTT
       1588 CGTATGCCGC         60
E--> 1590 GCCGCCAGGG GCTTTATAAA GGTCGTCCTG GGTACAGTTG GGATGGCTCC
       1591 ACGTTTCGGC        120
E--> 1593 TCTTAAGTGC AAGTGACTGC GAACATTTCG TTTGTTAGAA TAATTCAAGA
       1594 ATCGCTACCA        180
E--> 1596 ATCATGGATC C
W--> 1597 191
       1600 (2) INFORMATION FOR SEQ ID NO: 46:
       1602      (i) SEQUENCE CHARACTERISTICS:
       1603          (A) LENGTH: 167 base pairs
       1604          (B) TYPE: nucleic acid
       1605          (C) STRANDEDNESS: double
       1606          (D) TOPOLOGY: linear
       1608     (ii) MOLECULE TYPE: DNA (genomic)
       1610    (iii) HYPOTHETICAL: YES
       1612     (iv) ANTI-SENSE: NO
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1614      (vi) ORIGINAL SOURCE:
1615           (A) ORGANISM: Saccharomyces cerevisiae
1617      (ix) FEATURE:
1618           (A) NAME/KEY: promoter
1619           (B) LOCATION:8..167
1620           (C) IDENTIFICATION METHOD: experimental
1621           (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
1622 /standard_name= "Yeast promoter"
1623 /label= Yp15
1625      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:
E--> 1627 GAATTCGTGA CTCAGGGCCG TACTAAGTAG CTTTCGTATG CTATGCGGGG
     1628 TTTTATAAAT      60
E--> 1630 CTTTGGGCCA TGGTCTTGCT GGAAAACACC TCTCTTAAGT GCAAGTGACT
     1631 GCGAACATTT     120
E--> 1633 TTTTCGTTTG TTAGAATAAT TCAAGAATCG CTACCAATCA TGGATCC
W--> 1634 167
     1637 (2) INFORMATION FOR SEQ ID NO: 47:
     1639      (i) SEQUENCE CHARACTERISTICS:
     1640           (A) LENGTH: 191 base pairs
     1641           (B) TYPE: nucleic acid
     1642           (C) STRANDEDNESS: double
     1643           (D) TOPOLOGY: linear
     1645      (ii) MOLECULE TYPE: DNA (genomic)
     1647     (iii) HYPOTHETICAL: YES
     1649      (iv) ANTI-SENSE: NO
     1651      (vi) ORIGINAL SOURCE:
     1652           (A) ORGANISM: Saccharomyces cerevisiae
     1654      (ix) FEATURE:
     1655           (A) NAME/KEY: promoter
     1656           (B) LOCATION:8..191
     1657           (C) IDENTIFICATION METHOD: experimental
     1658           (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
     1659 /standard_name= "Yeast promoter"
     1660 /label= Yp154
     1662      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:
E--> 1664 GAATTCGTGA CTCACCGCTC GGGTGCAGGG CCAAGGCGGC GGAATGTGCG
     1665 GGGCGTTCTA      60
E--> 1667 GCGCAATCGG GGTATAAATT TATAAGGAGG CTGCGGGTGC TAGTTTGTCT
     1668 AGTTTGACTC     120
E--> 1670 TTAAGTGCAA GTGACTGCGA ACATTTTTCG TTTGTTAGAA TAATTCAAGA
     1671 ATCGCTACCA     180
E--> 1673 ATCATGGATC C
W--> 1674 191
     1677 (2) INFORMATION FOR SEQ ID NO: 48:
     1679      (i) SEQUENCE CHARACTERISTICS:
     1680           (A) LENGTH: 195 base pairs
     1681           (B) TYPE: nucleic acid
     1682           (C) STRANDEDNESS: double
     1683           (D) TOPOLOGY: linear
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 1685    (ii) MOLECULE TYPE: DNA (genomic)
 1687   (iii) HYPOTHETICAL: YES
 1689    (iv) ANTI-SENSE: NO
 1691    (vi) ORIGINAL SOURCE:
 1692         (A) ORGANISM: Saccharomyces cerevisiae
 1694    (ix) FEATURE:
 1695         (A) NAME/KEY: promoter
 1696         (B) LOCATION:8..190
 1697         (C) IDENTIFICATION METHOD: experimental
 1698         (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
 1699 /standard_name= "Yeast promoter"
 1700 /label= Yp18
 1702    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:
E--> 1704 GAATTCGTGA CTCAGGATTA GCTATGCCGG TTGGGATAAG CGAACAACTG
     1705 GAGGTGAGAA        60
E--> 1707 GCTTTTTGTC AGAATATAAA CCCGTTAGTC AGGGTTTGGT GGGATAGGGG
     1708 GTACTGTACC       120
E--> 1710 TCTTAAGTGC AAGTGACTGC GAACATTTTT TTCGTTTGTT AGAATAATTC
     1711 AAGAATCGCT       180
E--> 1713 ACCAATCATG GATCC
W--> 1714 195
```

VERIFICATION SUMMARY   DATE: 02/06/2001
PATENT APPLICATION: US/09/242,657B   TIME: 14:59:29

            Input Set : A:\Sequence Listing (55411.2).txt
            Output Set: N:\CRF3\02062001\I242657B.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:39 M:220 C: Keyword misspelled or invalid format, [(C) REFERENCE/DOCKET NUMBER:]
L:124 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:1
L:212 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:2
M:254 Repeated in SeqNo=2
L:216 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:303 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:3
M:254 Repeated in SeqNo=3
L:313 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:372 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:5
L:400 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:6
L:428 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:7
L:456 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:8
L:485 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:9
L:514 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:10
L:543 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:11
L:572 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:12
L:601 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:13
L:630 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:14
L:659 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:15
L:688 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:16
L:717 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:17
L:746 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:18
L:773 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:19
L:802 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:20
L:830 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:21
L:859 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:22
L:890 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:23
L:921 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:24
L:952 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:25
L:983 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:26
L:1014 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:27
L:1045 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:28
L:1076 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:29
L:1108 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:30
L:1139 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:31
L:1170 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:32
L:1201 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:33
L:1232 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:34
L:1263 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:35
L:1294 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:36
L:1325 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:37
L:1356 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:38
L:1387 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:39
L:1418 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:40
L:1449 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:41
L:1480 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:42

VERIFICATION SUMMARY   DATE: 02/06/2001
PATENT APPLICATION: US/09/242,657B   TIME: 14:59:29

            Input Set : A:\Sequence Listing (55411.2).txt
            Output Set: N:\CRF3\02062001\I242657B.raw

L:1510 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:43
M:254 Repeated in SeqNo=43
L:1517 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:43
L:1547 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:44
M:254 Repeated in SeqNo=44
L:1557 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44
L:1587 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:45
M:254 Repeated in SeqNo=45
L:1597 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:45
L:1627 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:46
L:1634 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:46
L:1674 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:47
L:1714 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:48
L:1791 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50
L:1831 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:51
L:1868 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52
L:1908 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53
L:1948 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:54
L:1988 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:55
L:2028 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:56
L:2068 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:57
L:2105 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:58